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Structure of βB2-crystallin in solution

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1 Introduction

The transparency of eye lens is maintained by the ordered arrangement of crystallins, which is a major component protein in the eye lens proteins. Based on reported reults eye lens crystallin is composed of three types of crytsallin: α- (45%), β- (20%) and γ-crystallin (35%). Among the above-described three types of crystallins only α-crystallin possesses chaperone functionality for preventing the formation of abnormal aggregates in the eye lens. On the other hand β- and γ-crystallins are the lens specific attained by exteremly high protein concentration. With aging these crystallins are graudually convered from native sate to abnormal aggregated state, leading to the onset of cataract. In order to undedatnd the onset of abnormal aggregation we have to unveil the mechnaim of aggregation process in solution state, which is relatively similar to in-vivo envrionement. Among the lens specific it is reported that crystallin βB2-crystallin is the dominant one . Hence thorugh the aggregation process of βB2-crystallin we have a chance to garsp the mechnaim of aggregation process in our lens. However even for the native state of βB2-crystallin the structure has not been determinned definitely.

Hence we tired to study the structure of native state of βB2-crystallin in solutiion state as a first step.

2 Experiment

We prepared human recombinant βB2-crystallin expressed by *E. coli*. Purified βB2-crystallin was dialyzed aginst 20 mM Tris/HCl, pH7.8 and 150 mM NaCl buffer. The concentration of βB2-crystallin was set to 3.5 mg/ml. The SAXS experiments were perfomed with a SAXS apparatus (SAXES) instlled at BL-10C of Photon Factory in Institute of Materials Structure Science, High Energy Accelerator Research Organization (KEK), Tsukuba, Japan at room temperature. The obaserved X-ray intensity was corrected for the buffer scattering and transmission. To avoid the sample damage by X-ray the irradiation time was limited to 10 sec.

3 Results and Discussion

Fig.1 shows SAXS profile of βB2-crystallin in native state. At first the radius of gyration (R_g) was evaluated form Guinier Analysis as shown by Fig.2. The evaluated R_g value was 22.9Å and compared to the R_g (=24.4Å) calculated from the crystal structure (1YTQ) solution structure exhibited compact structure. Referring to the crystal structure βB2-crystallin is composed of two domains (refer to the inset of Fig. 1), it is therefore expected that the two domains are closely packed. In order to further gain the structural difference between the crystal structure and that in solution state we calculated the scattering curve based on 1YTQ. In addition to the change of R_g high Q region was strongly deviated from experimental curve, which reinforces that solution structure is different from that in crystal. At present we try to fit the experimentally curve with the aid of MD simulation, which takes into account the dynamics of two domains. Referring to the preliminary result R_g is fluctuating with the elapse of time, indicating the domain motion in solution state. More precise data analysis is still on the progress.

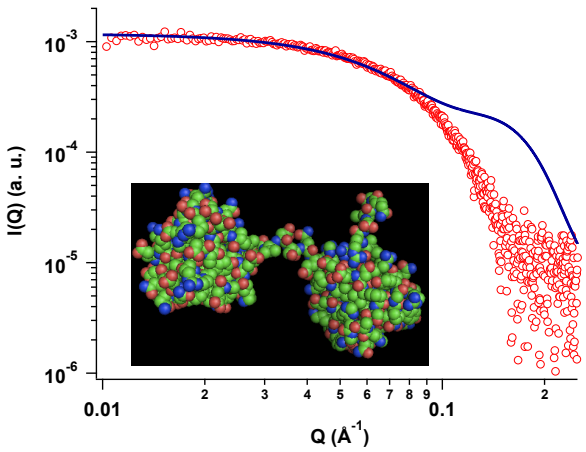

Fig. 1: Scattering profile of βB2-crystallin at room temperature and solid line corresponds to the simulated scattering curve based on its crystal structure. Inset indicates the crystal structure of βB2-crystallin.

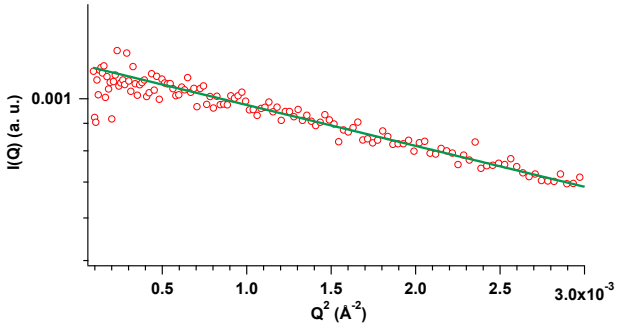

Fig. 2: Gunier plot of $I(Q)$ and solid line correspond to the result of fit with Guinier function.

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